

SCORE Search Results Details for Application 10537864 and Search Result 20071018_152746_us-10-537-864-2.p2n.mi.

| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
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This page gives you Search Results detail for the Application 10537864 and Search Result 20071018_152746_us-10-537-864-2.p2n.mi.

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GenCore version 6.2.1
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 18, 2007, 17:51:09 ; Search time 880 Seconds
 (without alignments)
 1170.640 Million cell updates/sec

Title: US-10-537-864-2
 Perfect score: 1442
 Sequence: 1 AASRSVAVAFLGLGLGVVC.....LLDPDQDATYFGAKFVKVLID 275

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310228

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

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-THR=4 -MODEL=frame+_p2n.model -DEV=SOFT
-Q=/abss/ABSSWEB_spool/US10537864/runat_18102007_152746_1847/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -SIMRANGE=0.0005
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=-1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=0 -MINLEN=0 -MAXLEN=2000000000 -MINDBSEQLEN=1 -HOST=ai2-01
-USER=US10537864@CGN_1_1_134@runat_18102007_152746_1847 -NCPU=6 -NO_MMAP
-NEG_SCORES=0 -WAIT -LONGLOG -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Issued_Patents_NA:*

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1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
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3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
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6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
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9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*
10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*
11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | | | | Description |
|---------------|-------|-------|--------|----|-------------------------------------|
| | Score | Match | Length | DB | |
| 1 | 1317 | 91.3 | 954 | 3 | US-08-996-139-12 Sequence 12, Appl |
| 2 | 1317 | 91.3 | 954 | 3 | US-08-995-659-12 Sequence 12, Appl |
| 3 | 1317 | 91.3 | 954 | 3 | US-09-215-649A-12 Sequence 12, Appl |
| 4 | 1317 | 91.3 | 954 | 3 | US-09-577-780-12 Sequence 12, Appl |
| 5 | 1317 | 91.3 | 954 | 3 | US-09-577-800-12 Sequence 12, Appl |
| 6 | 1317 | 91.3 | 954 | 3 | US-09-466-496-12 Sequence 12, Appl |
| 7 | 1317 | 91.3 | 954 | 3 | US-09-871-856-12 Sequence 12, Appl |
| 8 | 1317 | 91.3 | 954 | 3 | US-09-871-291-12 Sequence 12, Appl |
| 9 | 1317 | 91.3 | 954 | 3 | US-09-877-650-12 Sequence 12, Appl |
| 10 | 1317 | 91.3 | 954 | 3 | US-09-865-363-12 Sequence 12, Appl |
| 11 | 1317 | 91.3 | 954 | 3 | US-09-688-459-12 Sequence 12, Appl |
| 12 | 1317 | 91.3 | 954 | 3 | US-09-957-944-5 Sequence 5, Appl |
| 13 | 1317 | 91.3 | 954 | 5 | US-10-460-623-12 Sequence 12, Appl |
| 14 | 1317 | 91.3 | 2271 | 3 | US-09-052-521C-3 Sequence 3, Appl |
| 15 | 1317 | 91.3 | 2271 | 3 | US-09-396-937-1 Sequence 1, Appl |
| 16 | 1317 | 91.3 | 2271 | 5 | US-10-218-547A-21 Sequence 21, Appl |
| 17 | 1317 | 91.3 | 2271 | 5 | US-09-211-315A-38 Sequence 38, Appl |
| 18 | 1197 | 83.0 | 741 | 5 | US-10-460-623-19 Sequence 19, Appl |
| 19 | 1189 | 82.5 | 1630 | 3 | US-08-996-139-10 Sequence 10, Appl |
| 20 | 1189 | 82.5 | 1630 | 3 | US-08-995-659-10 Sequence 10, Appl |
| 21 | 1189 | 82.5 | 1630 | 3 | US-09-215-649A-10 Sequence 10, Appl |
| 22 | 1189 | 82.5 | 1630 | 3 | US-09-577-780-10 Sequence 10, Appl |
| 23 | 1189 | 82.5 | 1630 | 3 | US-09-577-800-10 Sequence 10, Appl |
| 24 | 1189 | 82.5 | 1630 | 3 | US-09-466-496-10 Sequence 10, Appl |
| 25 | 1189 | 82.5 | 1630 | 3 | US-09-871-856-10 Sequence 10, Appl |
| 26 | 1189 | 82.5 | 1630 | 3 | US-09-871-291-10 Sequence 10, Appl |
| 27 | 1189 | 82.5 | 1630 | 3 | US-09-877-650-10 Sequence 10, Appl |
| 28 | 1189 | 82.5 | 1630 | 3 | US-09-865-363-10 Sequence 10, Appl |
| 29 | 1189 | 82.5 | 1630 | 3 | US-09-688-459-10 Sequence 10, Appl |
| 30 | 1189 | 82.5 | 1694 | 3 | US-09-957-944-7 Sequence 7, Appl |
| 31 | 1189 | 82.5 | 1823 | 5 | US-10-017-910-1 Sequence 1, Appl |
| 32 | 1189 | 82.5 | 1823 | 5 | US-09-873-829-1 Sequence 1, Appl |
| 33 | 1182 | 82.0 | 951 | 3 | US-09-396-937-3 Sequence 3, Appl |
| 34 | 1182 | 82.0 | 951 | 5 | US-10-460-623-15 Sequence 15, Appl |
| 35 | 1182 | 82.0 | 1538 | 5 | US-10-460-623-2 Sequence 2, Appl |
| 36 | 1182 | 82.0 | 2191 | 3 | US-08-989-362-1 Sequence 1, Appl |

COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A
 FILING DATE: 17-Dec-1998
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 08/813,509
 FILING DATE: 07 MARCH 1997
 APPLICATION NUMBER: USSN 08/772,330
 FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 954 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

LIBRARY: <Unknown>
 CLONE: huRANKL (full length)

FEATURE:

NAME/KEY: CDS
 LOCATION: 1..951

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-215-649A-12

Alignment Scores:

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| Score: | 1317.00 | Matches: | 249 |
| Percent Similarity: | 94.5% | Conservative: | 11 |
| Best Local Similarity: | 90.5% | Mismatches: | 15 |
| Query Match: | 91.3% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-10-537-864-2 (1-275) x US-09-215-649A-12 (1-954)

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 Qy 201 ThrLysThrSerIleLysIleProSerSerHisThrLeuMetLysGlyGlySerThrLys 220
 Db 727 ACTAAAACCAGCATAAAATCCCAAGTTCTCATACCCGTGAAAGGAGGAAGCACCAAG 786
 Qy 221 TyrTrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 240
 Db 787 TATTGGTCAGGGAAATTCTGAATTCCATTTCATTCCATAAACGTTGGATTTTTAAG 846
 Qy 241 LeuArgSerGlyGluGluIleSerIleGluValSerAsnProSerLeuLeuAspProAsp 260
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 Qy 261 GlnAspAlaThrTyrPheGlyAlaPheLysValLeuAspIleAsp 275
 Db 907 CAGGATGCAACATACTTGGGCCTTAAAGTCGAGATATAGAT 951

RESULT 14

US-09-052-521C-3

; Sequence 3, Application US/09052521C
 ; Patent No. 6316408
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 ; FILE REFERENCE: A-451Brv
 ; CURRENT APPLICATION NUMBER: US/09/052,521C
 ; CURRENT FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 08/880,855
 ; PRIOR FILING DATE: 1997-06-23
 ; PRIOR APPLICATION NUMBER: 08/842,842
 ; PRIOR FILING DATE: 1997-04-16
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 2271
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (185)..(1135)

US-09-052-521C-3

Alignment Scores:

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|------------------------|-----------|---------------|------|
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| Best Local Similarity: | 90.5% | Mismatches: | 15 |
| Query Match: | 91.3% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-10-537-864-2 (1-275) x US-09-052-521C-3 (1-2271)

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| | |
|----|--|
| Qy | 21 SerValAlaLeuPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsp 40 |
| Db | 371 AGCGTCGCCCTGGTTCTCTATTTCAAGAGCGCAGATGGATCCTAATAGAATATCAGAAGAT 430 |
| Qy | 41 AspThrHisCysIleAsnArgIlePheLysLeuHisGluAsnAlaAspLeuGlnAspThr 60 :::: |
| Db | 431 GGCACTCACTGCATTATAGAATTGGAGACTCCATGAAAATGCAAGATTTCAGACACACA 490 |
| Qy | 61 ThrLeuGluAsnGlnAspThrLysLeuIleProAspSerCysLysSerIleLysGlnAla 80 :: :: :: |
| Db | 491 ACTCTGGAGAGTCAGAATACAAATTAACTGATCATGTAGGAGAATTAAACAGGCC 550 |
| Qy | 81 PheArgAlaAlaValGlnLysGluLeuGlnHisIleValArgSerGlnHisIleArgAla 100 ::: |
| Db | 551 TTTCAGGAGCTGTCAAAGGAATTACAACATATCGTTGGATCACAGCACATCAGAGCA 610 |
| Qy | 101 GluLysAlaMetMetGluGlySerTrpLeuGluMetAlaArgArgGlyLysThrHisThr 120 :::: :::: |
| Db | 611 GAGAAAGCGATGGTGATGGCTCATGGTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCT 670 |
| Qy | 121 GlnProPheAlaHisLeuThrIleAsnAlaThrAspIleProSerGlySerHisLysVal 140 |
| Db | 671 CAGCCTTTGCTCATCTCACTATTATGCCACCACATCCCCTGTTCCATAAAAGTG 730 |
| Qy | 141 SerLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrPheSer 160 |
| Db | 731 AGTCTGCTCTGGTACCATGATGGGGTTGGGCCAAGATCTCAACATGACTTTAGC 790 |
| Qy | 161 AsnGlyLysLeuIleValAsnGlnAspGlyPheTyrPheLeuTyrAlaAsnIleCysPhe 180 :: |
| Db | 791 AATGGAAAACTAATAGTTAACAGGATGGCTTTATTACCTGTATGCCAACATTGCTT 850 |
| Qy | 181 ArgHisHisGluThrSerGlyAspLeuAlaThrGluTyrLeuGlnLeuMetValTyrVal 200 |
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| Db | 911 ACTAAAACCAGCATAAAATCCAAAGTTCTCATACCCGTGAAAGGGAGGAAGCACCAAG 970 |
| Qy | 221 TyrTrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 240 |
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| Qy | 241 LeuArgSerGlyGluGluIleSerIleGluValSerAsnProSerIleLeuAspProAsp 260 |
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| Qy | 261 GlnAspAlaThrTyrPheGlyAlaPheLysValLeuAspIleAsp 275 |
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RESULT 15

US-09-396-937-1

; Sequence 1, Application US/09396937

; Patent No. 6645500